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SEQUENCE LISTING

<110> Lipton, Stuart A.
Okamoto, Shu-ichi

<120> Methods of Differentiating and
Protecting Cells By Modulating the P38/MEF2 Pathway

<130> P-LJ 4714

<140> US 09/876,187

<141> 2001-06-05

<150> US 60/209,539

<151> 2000-06-05

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<170> FastSEQ for Windows Version 4.0

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<211> 2975

<212> DNA

<213> Homo sapiens

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<221> CDS

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Met

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Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr
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gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc aac 561
Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn
35 40 45

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ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc aac	657
Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn	
70 75 80	
tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc gac	705
Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp	
85 90 95	
agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa gaa	753
Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu	
100 105 110	
aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat cat	801
Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His	
115 120 125	
aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca	849
Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr	
130 135 140 145	
gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg agt	897
Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser	
150 155 160	
tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat tca	945
Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser	
165 170 175	
agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct cct	993
Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro	
180 185 190	
gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg ttg	1041
Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu	
195 200 205	
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Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val	
210 215 220 225	
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Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala	
230 235 240	
act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc cct	1185
Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro Pro	
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cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat ctt	1233
Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp Leu	
260 265 270	
cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta tcg	1281
Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser	
275 280 285	
gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct caa	1329
Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser Gln	
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310 315 320	
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Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn	
325 330 335	
act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc ttc	1473
Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly Phe	
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Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln Gln	
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His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln	
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tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc	1617
Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser	
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atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca tcg	1665
Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser	
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Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro	
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Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro Ile
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Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser Val
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Lys Arg Met Arg Met Asp Ala Trp Val Thr
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35 40 45
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
50 55 60
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
65 70 75 80
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
85 90 95
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
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agcatgtgcg tcgtccctc cccgagctgg ccagacacaa ggcagacatg cagcgttggg 180
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cctcagcctg atcctggaag agactcgggg ccccccagcc tccgccaacc cagacaaaga 420
tcattccact cagcctggga cg atg ggg agg aaa aaa atc cag atc tcc cgc 472
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atc ctg gac caa agg aat cgg cag gtg acg ttc acc aag cgg aag ttc 520
Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe
          15             20             25

ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag 568
Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu
          30             35             40

ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc 616
Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala
          45             50             55

agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag 664
Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu
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ccc cac gag agc cgc acc aac act gac atc ctc gag acg ctg aag cgg 712
Pro His Glu Ser Arg Thr Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg
          75             80             85             90

agg ggc att ggc ctc gat ggg cca gag ctg gag ccg gat gaa ggg cct 760
Arg Gly Ile Gly Leu Asp Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro
          95             100             105

gag gag cca gga gag aag ttt cgg agg ctg gca ggc gaa ggg ggt gat 808
Glu Glu Pro Gly Glu Lys Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp
          110             115             120

ccg gcc ttg ccc cga ccc cgg ctg tat cct gca gct cct gct atg ccc 856
Pro Ala Leu Pro Arg Pro Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro
          125             130             135

agc cca gat gtg gta tac ggg gcc tta ccg cca cca ggc tgt gac ccc 904
Ser Pro Asp Val Val Tyr Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro
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cga cca gca gcc ccc aaa gcc ggg ccc cca ggc ctg gtg cac cct ctc	1000
Arg Pro Ala Ala Pro Lys Ala Gly Pro Pro Gly Leu Val His Pro Leu	
175 180 185	
ttc tca cca agc cac ctc acc agc aag aca cca ccc cca ctg tac ctg	1048
Phe Ser Pro Ser His Leu Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu	
190 195 200	
ccg acg gaa ggg cgg agg tca gac ctg cct ggt ggc ctg gct ggg ccc	1096
Pro Thr Glu Gly Arg Arg Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro	
205 210 215	
cga ggg gga cta aac acc tcc aga agc ctc tac agt ggc ctg cag aac	1144
Arg Gly Gly Leu Asn Thr Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn	
220 225 230	
ccc tgc tcc act gca act ccc gga ccc cca ctg ggg agc ttc ccc ttc	1192
Pro Cys Ser Thr Ala Thr Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe	
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ctc ccc gga ggc ccc cca gtg ggg gcc gaa gcc tgg gcg agg agg gtc	1240
Leu Pro Gly Gly Pro Pro Val Gly Ala Glu Ala Trp Ala Arg Arg Val	
255 260 265	
ccc caa ccc gcg gcg cct ccc cgc cga ccc ccc cag tca gca tca agt	1288
Pro Gln Pro Ala Ala Pro Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser	
270 275 280	
ctg agc gcc tct ctc cgg ccc ccg ggg gcc ccg gcg act ttc cta aga	1336
Leu Ser Ala Ser Leu Arg Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg	
285 290 295	
cct tcc cct atc cct tgc tcc tcg ccc ggt ccc tgg cag agc ctc tgc	1384
Pro Ser Pro Ile Pro Cys Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys	
300 305 310	
ggc ctg ggc ccg ccc tgc gcc ggc tgc cct tgg ccg acg gct ggc ccc	1432
Gly Leu Gly Pro Pro Cys Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro	
315 320 325 330	
ggt agg aga tca ccc ggt ggc acc agc cca gag cgc tcg cca ggt acg	1480
Gly Arg Arg Ser Pro Gly Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr	
335 340 345	
gcg agg gca cgt ggg gac ccc acc tcc ctc cag gcc tct tca gag aag	1528
Ala Arg Ala Arg Gly Asp Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys	
350 355 360	
acc caa cag tgacgcccc ctccgcggtg ggggcttgga ggtgggcggc	1577

Thr Gln Gln
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35 40 45
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
50 55 60
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
65 70 75 80
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp
85 90 95
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys
100 105 110
Phe Arg Arg Leu Ala Gly Glu Gly Asp Pro Ala Leu Pro Arg Pro
115 120 125
Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr
130 135 140
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala
145 150 155 160
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys
165 170 175
Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu
180 185 190
Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg
195 200 205
Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr
210 215 220
Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
225 230 235 240
Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
245 250 255
Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
260 265 270
Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
275 280 285
Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
290 295 300
Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
305 310 315 320
Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly

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<222> (402)...(1820)

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gttatttttt ttttctctct ctctctctct taagaaagga aaatatccca aggactaatc 240
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gctgaagaag gagatttggt tggaggaaac aggaaagaga aagaaaagga aggaaaaaat 360
acataatttc agggacgaga gagagaagaa aaacggggac t atg ggg aga aaa aag 416
                                         Met Gly Arg Lys Lys
                                         1             5

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att cag att acg agg att atg gat gaa cgt aac aga cag gtg aca ttt 464
Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg Gln Val Thr Phe
                        10                15                20

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aca aag agg aaa ttt ggg ttg atg aag aag gct tat gag ctg agc gtg 512
Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val
                        25                30                35

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ctg tgt gac tgt gag att gcg ctg atc atc ttc aac agc acc aac aag 560
Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn Ser Thr Asn Lys
                        40                45                50

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ctg ttc cag tat gcc agc acc gac atg gac aaa gtg ctt ctc aag tac 608
Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val Leu Leu Lys Tyr
                        55                60                65

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acg gag tac aac gag ccg cat gag agc cgg aca aac tca gac atc gtg 656
Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn Ser Asp Ile Val
                        70                75                80                85

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gag acg ttg aga aag aag ggc ctt aat ggc tgt gac agc cca gac ccc 704
Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys Asp Ser Pro Asp Pro
                        90                95                100

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120	125	130	
tgt gct gtt cca cct ccc aac ttc gag atg cca gtc tcc atc cca gtg			848
Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro Val Ser Ile Pro Val			
135	140	145	
tcc agc cac aac agt ttg gtg tac agc aac cct gtc agc tca ctg gga			896
Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro Val Ser Ser Leu Gly			
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aac ccc aac cta ttg cca ctg gct cac cct tct ctg cag agg aat agt			944
Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser Leu Gln Arg Asn Ser			
170	175	180	
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Met Ser Pro Gly Val Thr His Arg Pro Pro Ser Ala Gly Asn Thr Gly			
185	190	195	
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Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala Gly Thr Ser Ala Gly			
200	205	210	
aac ggg tat ggc aat ccc cga aac tca cca ggt ctg ctg gtc tca cct			1088
Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly Leu Leu Val Ser Pro			
215	220	225	
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Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser Pro Pro Pro Met Asn			
230	235	240	245
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Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu Ile Pro Pro			
250	255	260	
ggc agc aag aat acg atg cca tca gtg tct gag gat gtc gac ctg ctt			1232
Gly Ser Lys Asn Thr Met Pro Ser Val Ser Glu Asp Val Asp Leu Leu			
265	270	275	
ttg aat caa agg ata aat aac tcc cag tcg gct cag tca ttg gct acc			1280
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Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly			
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Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu			
310	315	320	325

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Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala
330 335 340

ctt cac ctt ggt tca gta act ggc tgg caa cag caa cac cta cat aac 1472
Leu His Leu Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn
345 350 355

atg cca cca tct gcc ctc agt cag ttg gga gct tgc act agc act cat 1520
Met Pro Pro Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His
360 365 370

tta tct cag agt tca aat ctc tcc ctg cct tct act caa agc ctc aac 1568
Leu Ser Gln Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn
375 380 385

atc aag tca gaa cct gtt tct cct cct aga gac cgt acc acc acc cct 1616
Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro
390 395 400 405

tcg aga tac cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt 1664
Ser Arg Tyr Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val
410 415 420

gac agc ttg agc agc tgt agc agt tcg tac gac ggg agc gac cga gag 1712
Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu
425 430 435

gat cac cgg aac gaa ttc cac tcc ccc att gga ctc acc aga cct tcg 1760
Asp His Arg Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser
440 445 450

ccg gac gaa agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa 1808
Pro Asp Glu Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu
455 460 465

gga tgg gca aca tgatecagatt attacttact agtttttttt tttttcttgc 1860
Gly Trp Ala Thr
470

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Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
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<212> DNA

<213> Homo sapiens

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Glu Ser Arg Thr Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly	
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Phe Asn Gly Cys Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu	
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Gln Ser Pro Leu Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu	
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Asp Gly Leu Phe Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe	
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Pro Pro Pro Thr His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro	
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Ser Asn Leu Ile Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu
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Pro Ser Arg Glu Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro
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gct gcc cgc cct gag cct ggc gat ggt ctc agc agc cca gcc ggg gga 1623
Ala Ala Arg Pro Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly
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495 500 505

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Ala Val Lys Arg Met Arg Leu Asp Thr Trp Thr Leu Lys *
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Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe
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Pro	Gly	Leu	Pro	Gln	Arg	Pro	Ala	Ser	Ala	Gly	Ala	Met	Leu	Gly	Gly	195	200	205
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Tyr	Val	Ser	Ala	Arg	Ala	Ser	Pro	Gly	Leu	Leu	Pro	Val	Ala	Asn	Gly	225	230	235
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His	Ser	Thr	Gln	Leu	Gly	Ala	Pro	Ser	Arg	Lys	Pro	Asp	Leu	Arg	Val	260	265	270
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Pro	Gln	Gln	Gln	Ser	His	Leu	Val	Pro	Val	Ser	Leu	Ser	Asn	Leu	Ile	405	410	415
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Gly	Asp	Arg	Asp	Asp	Gly	Arg	Gly	Asp	Phe	Gly	Pro	Thr	Leu	Gly	Leu	485	490	495
Leu	Arg	Pro	Ala	Pro	Glu	Pro	Glu	Ala	Glu	Gly	Ser	Ala	Val	Lys	Arg	500	505	510
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